

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>
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SERIAL NUMBER: 09/981,649

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 **Misaligned Amino Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 **PatentIn 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 **Skipped Sequences (OLD RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
- Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 **Skipped Sequences (NEW RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ✓ **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n of Xaa, and which residue n or Xaa represents.
- 10 **Invalid <213> Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 **Use of <220>** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 **PatentIn 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/981,649

DATE: 11/13/2001

TIME: 10:33:44

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\11132001\I981649.raw

**Does Not Comply
Corrected Diskette Needed**

2 <110> APPLICANT: Asundi, Vinod
 3 Ford, John E.
 4 Drmanac, Radoje T.
 5 Liu, Chenghua
 6 Tang, Y. Tom
 7 Yamasaki, Vicky
 8 Yeung, George
 9 Zhang, Jie
 10 Zhou, Ping
 11 Zhou, Hua

W--> 12 <120> TITLE OF INVENTION: EGF MOTIF PROTEIN, EGFL6, MATERIALS AND METHODS
 W--> 13 <130> FILE REFERENCE: 28110/37665
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/981,649
 C--> 14 <141> CURRENT FILING DATE: 2001-10-15
 14 <150> PRIOR APPLICATION NUMBER: US 09/687,860
 15 <151> PRIOR FILING DATE: 2000-10-13
 16 <150> PRIOR APPLICATION NUMBER: US 09/620,312
 17 <151> PRIOR FILING DATE: 2000-07-19
 18 <150> PRIOR APPLICATION NUMBER: US 09/363,316
 19 <151> PRIOR FILING DATE: 1999-07-28

W--> 20 <160> NUMBER OF SEQ ID: 32
 21 <170> SOFTWARE: FastSEQ for Windows Version 3.0

W--> 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 300
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens

W--> 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (1)...(300)
 29 <221> NAME/KEY: misc_feature
 30 <222> LOCATION: (1)...(300)
 31 <223> OTHER INFORMATION: n = A, T, C or G

W--> 32 <400> SEQUENCE: 1

33	ggc tgg aga aga aac agc aag gga gtc tgt gaa gct aca tgc gaa cct	48
34	Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro	
35	1 5 10 15	
37	gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt	96
38	Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe	
39	20 25 30	
41	cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga	144
42	Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly	
43	35 40 45	
45	atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc	192
46	Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser	
47	50 55 60	
49	tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg	240
50	Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr	

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

see error summary sheet, Item 9

- explanation was not given for Xaa

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```

51      65      70      75      80
W--> 53  tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt      288
W--> 54  Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
55      85      90      95
56  gaa gac aca gaa      300
57  Glu Asp Thr Glu
58      100
60 <210> SEQ ID NO: 2
61 <211> LENGTH: 1611
62 <212> TYPE: DNA
63 <213> ORGANISM: Homo sapiens
W--> 64 <220> FEATURE:
65 <221> NAME/KEY: CDS
66 <222> LOCATION: (1)...(1506)
67 <221> NAME/KEY: misc_feature
68 <222> LOCATION: (1)...(1611)
69 <223> OTHER INFORMATION: n = A,T,C or G
W--> 70 <400> SEQUENCE: 2
71  ggc tgg aga aga aac agc aag gga gtc tgt gaa gct aca tgc gaa cct      48
72  Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
73  1      5      10      15
75  gga tgt aag ttt ggt gag tgc gtg gga cca aac aaa tgc aga tgc ttt      96
76  Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
77      20      25      30
79  cca gga tac acc ggg aaa acc tgc agt caa gat gtg aat gag tgt gga      144
80  Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
81      35      40      45
83  atg aaa ccc cgg cca tgc caa cac aga tgt gtg aat aca cac gga agc      192
84  Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
85      50      55      60
87  tac aag tgc ttt tgc ctc agt ggc cac atg ctc atg cca gat gct acg      240
88  Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
89  65      70      75      80
W--> 91  tgt gtg aac tcn agg aca tgt gcc atg ata aac tgt cag tat agc tgt      288
W--> 92  Cys Val Asn Xaa Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
93      85      90      95
95  gaa gac aca gaa gaa ggg cca cag tgc ctg tgt cca tcc tca gga ctc      336
96  Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu
97      100      105      110
99  cgc ctg gcc cca aat gga aga gac tgt cta gat att gat gaa tgt gcc      384
100  Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala
101      115      120      125
103  tct ggt aaa gtc atc tgt ccc tac aat cga aga tgt gtg aac aca ttt      432
104  Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe
105      130      135      140
106  gga agc tac tac tgc aaa tgt cac att ggt ttc gaa ctg caa tat atc      480
107  Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile
108  145      150      155      160
110  agt gga cga tat gac tgt ata gat ata aat gaa tgt act atg gat agc      528

```

- same error

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111	Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser	
112	165 170 175	
114	cat acg tgc agc cac cat gcc aat tgc ttc aat acc caa ggg tcc ttc	576
115	His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe	
116	180 185 190	
118	aag tgt aaa tgc aag cag gga tat aaa ggc aat gga ctt cgg tgt tct	624
119	Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser	
120	195 200 205	
122	gct atc cct gaa aat tct gtg aag gaa gtc ctc aga gca cct ggt acc	672
123	Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr	
124	210 215 220	
126	atc aaa gac aga atc aag aag ttg ctt gct cac aaa aac agc atg aaa	720
127	Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys	
128	225 230 235 240	
130	aag aag gca aaa att aaa aat gtt acc cca gaa ccc acc agg act cct	768
131	Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro	
132	245 250 255	
134	acc cct aag gtg aac ttg cag ccc ttc aac tat gaa gag ata gtt tcc	816
135	Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser	
136	260 265 270	
138	aga ggc ggg aac tct cat gga ggt aaa aaa ggg aat gaa gag aaa atg	864
139	Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met	
140	275 280 285	
142	aaa gag ggg ctt gag gat gag aaa aga gaa gag aaa gcc ctg aag aat	912
143	Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn	
144	290 295 300	
146	gac ata gag gag cga agc ctg cga gga gat gtg ttt ttc cct aag gtg	960
147	Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val	
148	305 310 315 320	
150	aat gaa gca ggt gaa ttc ggc ctg att ctg gtc caa agg aaa gcg cta	1008
151	Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu	
152	325 330 335	
154	act tcc aaa ctg gaa cat aaa gat tta aat atc tcg gtt gac tgc agc	1056
155	Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser	
156	340 345 350	
158	ttc aat cat ggg atc tgt gac tgg aaa cag gat aga gaa gat gat ttt	1104
159	Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe	
160	355 360 365	
161	gac tgg aat cct gct gat cga gat aat gct att ggc ttc tat atg gca	1152
162	Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala	
163	370 375 380	
165	gtt ccg gcc ttg gca ggt cac atg aaa gac att ggc cga ttg aaa ctt	1200
166	Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu	
167	385 390 395 400	
169	ctc cta cct gac ctg caa ccc caa agc aac ttc tgt ttg ctc ttt gat	1248
170	Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp	
171	405 410 415	
173	tac cgg ctg gcc gga gac aaa gtc ggg aaa ctt cga gtg ttt gtg aaa	1296
174	Tyr Arg Leu Ala Gly Asp Lys Val Gly Lys Leu Arg Val Phe Val Lys	

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```

175          420          425          430
177 aac agt aac aat gcc ctg gca tgg gag aag acc acg agt gag gat gaa 1344
178 Asn Ser Asn Asn Ala Leu Ala Trp Glu Lys Thr Thr Ser Glu Asp Glu
179          435          440          445
181 aag tgg aag aca ggg aaa att cag ttg tat caa gga act gat gct acc 1392
182 Lys Trp Lys Thr Gly Lys Ile Gln Leu Tyr Gln Gly Thr Asp Ala Thr
183          450          455          460
185 aaa agc atc att ttt gaa gca gaa cgt ggc aag ggc aaa acc ggc gaa 1440
186 Lys Ser Ile Ile Phe Glu Ala Glu Arg Gly Lys Gly Lys Thr Gly Glu
187          465          470          475          480
189 atc gca gtg gat ggc gtc ttg ctt gtt tca ggc tta tgt cca gat agc 1488
190 Ile Ala Val Asp Gly Val Leu Leu Val Ser Gly Leu Cys Pro Asp Ser
191          485          490          495
W--> 193 ctt tta tct gtg gan nnc tgaatggtac tatctttata tttgactttg 1536
W--> 194 Leu Leu Ser Val Xaa Xaa same error
195          500
197 tatgtcagtt ccctggtttt tttgatattg catcatagga cctctggcat tttaaaatta 1596
198 ctagctgaaa aattg 1611
199 <210> SEQ ID NO: 3
200 <211> LENGTH: 100
201 <212> TYPE: PRT
202 <213> ORGANISM: Homo sapiens
W--> 203 <400> SEQUENCE: 3
204 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
205 1 5 10 15
206 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe
207 20 25 30
208 Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly
209 35 40 45
210 Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser
211 50 55 60
212 Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr
213 65 70 75 80
214 Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys
215 85 90 95
216 Glu Asp Thr Glu
217 100
218 <210> SEQ ID NO: 4
219 <211> LENGTH: 537
220 <212> TYPE: PRT
221 <213> ORGANISM: Homo sapiens
W--> 222 <220> FEATURE:
223 <221> NAME/KEY: VARIANT
224 <222> LOCATION: (1)...(537)
225 <223> OTHER INFORMATION: Xaa = Any Amino Acid
W--> 226 <400> SEQUENCE: 4
227 Gly Trp Arg Arg Asn Ser Lys Gly Val Cys Glu Ala Thr Cys Glu Pro
228 1 5 10 15
230 Gly Cys Lys Phe Gly Glu Cys Val Gly Pro Asn Lys Cys Arg Cys Phe

```

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231		20		25		30	
232	Pro Gly Tyr Thr Gly Lys Thr Cys Ser Gln Asp Val Asn Glu Cys Gly						
233		35		40		45	
234	Met Lys Pro Arg Pro Cys Gln His Arg Cys Val Asn Thr His Gly Ser						
235		50		55		60	
236	Tyr Lys Cys Phe Cys Leu Ser Gly His Met Leu Met Pro Asp Ala Thr						
237	65		70		75		80
238	Cys Val Asn Ser Arg Thr Cys Ala Met Ile Asn Cys Gln Tyr Ser Cys						
239		85		90		95	
240	Glu Asp Thr Glu Glu Gly Pro Gln Cys Leu Cys Pro Ser Ser Gly Leu						
241		100		105		110	
242	Arg Leu Ala Pro Asn Gly Arg Asp Cys Leu Asp Ile Asp Glu Cys Ala						
243		115		120		125	
244	Ser Gly Lys Val Ile Cys Pro Tyr Asn Arg Arg Cys Val Asn Thr Phe						
245		130		135		140	
246	Gly Ser Tyr Tyr Cys Lys Cys His Ile Gly Phe Glu Leu Gln Tyr Ile						
247	145		150		155		160
248	Ser Gly Arg Tyr Asp Cys Ile Asp Ile Asn Glu Cys Thr Met Asp Ser						
249		165		170		175	
250	His Thr Cys Ser His His Ala Asn Cys Phe Asn Thr Gln Gly Ser Phe						
251		180		185		190	
252	Lys Cys Lys Cys Lys Gln Gly Tyr Lys Gly Asn Gly Leu Arg Cys Ser						
253		195		200		205	
254	Ala Ile Pro Glu Asn Ser Val Lys Glu Val Leu Arg Ala Pro Gly Thr						
255		210		215		220	
256	Ile Lys Asp Arg Ile Lys Lys Leu Leu Ala His Lys Asn Ser Met Lys						
257	225		230		235		240
258	Lys Lys Ala Lys Ile Lys Asn Val Thr Pro Glu Pro Thr Arg Thr Pro						
259		245		250		255	
260	Thr Pro Lys Val Asn Leu Gln Pro Phe Asn Tyr Glu Glu Ile Val Ser						
261		260		265		270	
262	Arg Gly Gly Asn Ser His Gly Gly Lys Lys Gly Asn Glu Glu Lys Met						
263		275		280		285	
264	Lys Glu Gly Leu Glu Asp Glu Lys Arg Glu Glu Lys Ala Leu Lys Asn						
265		290		295		300	
267	Asp Ile Glu Glu Arg Ser Leu Arg Gly Asp Val Phe Phe Pro Lys Val						
268	305		310		315		320
269	Asn Glu Ala Gly Glu Phe Gly Leu Ile Leu Val Gln Arg Lys Ala Leu						
270		325		330		335	
271	Thr Ser Lys Leu Glu His Lys Asp Leu Asn Ile Ser Val Asp Cys Ser						
272		340		345		350	
273	Phe Asn His Gly Ile Cys Asp Trp Lys Gln Asp Arg Glu Asp Asp Phe						
274		355		360		365	
275	Asp Trp Asn Pro Ala Asp Arg Asp Asn Ala Ile Gly Phe Tyr Met Ala						
276		370		375		380	
277	Val Pro Ala Leu Ala Gly His Met Lys Asp Ile Gly Arg Leu Lys Leu						
278	385		390		395		400
279	Leu Leu Pro Asp Leu Gln Pro Gln Ser Asn Phe Cys Leu Leu Phe Asp						
280		405		410		415	

VERIFICATION SUMMARY

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Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\11132001\I981649.raw

L:12 M:283 W: Missing Blank Line separator, <120> field identifier
L:13 M:283 W: Missing Blank Line separator, <130> field identifier
L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:20 M:283 W: Missing Blank Line separator, <160> field identifier
L:22 M:283 W: Missing Blank Line separator, <210> field identifier
L:26 M:283 W: Missing Blank Line separator, <220> field identifier
L:32 M:283 W: Missing Blank Line separator, <400> field identifier
L:53 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:64 M:283 W: Missing Blank Line separator, <220> field identifier
L:70 M:283 W: Missing Blank Line separator, <400> field identifier
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:203 M:283 W: Missing Blank Line separator, <400> field identifier
L:222 M:283 W: Missing Blank Line separator, <220> field identifier
L:226 M:283 W: Missing Blank Line separator, <400> field identifier
L:291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:302 M:283 W: Missing Blank Line separator, <220> field identifier
L:305 M:283 W: Missing Blank Line separator, <400> field identifier
L:396 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:450 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:462 M:283 W: Missing Blank Line separator, <220> field identifier
L:466 M:283 W: Missing Blank Line separator, <400> field identifier
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:542 M:283 W: Missing Blank Line separator, <220> field identifier
L:546 M:283 W: Missing Blank Line separator, <400> field identifier
L:547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:557 M:283 W: Missing Blank Line separator, <220> field identifier
L:561 M:283 W: Missing Blank Line separator, <400> field identifier
L:562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:564 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:572 M:283 W: Missing Blank Line separator, <400> field identifier
L:599 M:283 W: Missing Blank Line separator, <220> field identifier
L:603 M:283 W: Missing Blank Line separator, <400> field identifier
L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:606 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:614 M:283 W: Missing Blank Line separator, <220> field identifier
L:618 M:283 W: Missing Blank Line separator, <400> field identifier
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:631 M:283 W: Missing Blank Line separator, <220> field identifier

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Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\11132001\I981649.raw

L:633 M:283 W: Missing Blank Line separator, <400> field identifier
L:639 M:283 W: Missing Blank Line separator, <220> field identifier
L:641 M:283 W: Missing Blank Line separator, <400> field identifier
L:647 M:283 W: Missing Blank Line separator, <220> field identifier
L:649 M:283 W: Missing Blank Line separator, <400> field identifier
L:655 M:283 W: Missing Blank Line separator, <220> field identifier
L:657 M:283 W: Missing Blank Line separator, <400> field identifier
L:663 M:283 W: Missing Blank Line separator, <220> field identifier
L:665 M:283 W: Missing Blank Line separator, <400> field identifier
L:671 M:283 W: Missing Blank Line separator, <220> field identifier
L:673 M:283 W: Missing Blank Line separator, <400> field identifier
L:679 M:283 W: Missing Blank Line separator, <220> field identifier
L:683 M:283 W: Missing Blank Line separator, <400> field identifier
L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:752 M:283 W: Missing Blank Line separator, <220> field identifier
L:754 M:283 W: Missing Blank Line separator, <400> field identifier
L:760 M:283 W: Missing Blank Line separator, <220> field identifier
L:762 M:283 W: Missing Blank Line separator, <400> field identifier
L:768 M:283 W: Missing Blank Line separator, <220> field identifier
L:778 M:283 W: Missing Blank Line separator, <220> field identifier
L:788 M:283 W: Missing Blank Line separator, <220> field identifier
L:791 M:283 W: Missing Blank Line separator, <400> field identifier
L:913 M:283 W: Missing Blank Line separator, <220> field identifier
L:992 M:283 W: Missing Blank Line separator, <220> field identifier
L:994 M:283 W: Missing Blank Line separator, <400> field identifier
L:1001 M:283 W: Missing Blank Line separator, <220> field identifier
L:1017 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1025 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1028 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1031 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1034 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1037 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1040 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1043 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1046 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1049 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1052 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1055 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1058 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1061 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1064 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1067 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1071 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1074 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1077 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1080 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1083 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1086 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1089 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/981,649

DATE: 11/13/2001

TIME: 10:33:45

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\11132001\I981649.raw

L:1092 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1095 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1098 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1122 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1125 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1128 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1232 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1235 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1238 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1241 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1244 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1247 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1250 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1253 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1256 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1265 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1268 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29

TIME: 15:12:26

Output Set: N:\CRF3\11022001\I981649.raw

Does Not Comply
Corrected Diskette Needed

Corrected Disk

2 <110> APPLICANT: Asundi, Vinod
3 Ford, John E.
4 Drmanac, Radoje T.
5 Liu, Chenghua
6 Tang, Y. Tom
7 Yamasaki, Vicky
8 Yeung, George
9 Zhang, Jie
10 Zhou, Ping
11 Zhou, Hua

W--> 12 <120> TITLE OF INVENTION: EGF MOTIF PROTEIN, EGFL6, MATERIALS AND METHODS
W--> 13 <130> FILE REFERENCE: 28110/37665
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/981,649
C--> 14 <141> CURRENT FILING DATE: 2001-10-15
14 <150> PRIOR APPLICATION NUMBER: US 09/687,860
15 <151> PRIOR FILING DATE: 2000-10-13
16 <150> PRIOR APPLICATION NUMBER: US 09/620,312
17 <151> PRIOR FILING DATE: 2000-07-19
18 <150> PRIOR APPLICATION NUMBER: US 09/363,316
19 <151> PRIOR FILING DATE: 1999-07-28

W--> 20 <160> NUMBER OF SEQ ID: 32
21 <170> SOFTWARE: FastSEQ for Windows Version 3.0

```

772 <210> SEQ ID NO: 22
773 <211> LENGTH: 20
774 <212> TYPE: DNA
775 <213> ORGANISM: Artificial Sequence

```

```
W--> 776 <220> FEATURE:
      777 <223> OTHER INFORMATION: Description of Artificial Sequence: primer
```

W--> 778 <400> SEQUENCE: 22

E--> 779 qggaactqac atacaaaqtc

→ 22 ~~was~~ ^{must be} added at the end of the line
(no. of nucleotides)

VERIFICATION SUMMARY

DATE: 11/02/2001

PATENT APPLICATION: US/09/981,649

TIME: 15:12:27

Input Set : A:\37665seq.txt

Output Set: N:\CRF3\11022001\I981649.raw

L:12 M:283 W: Missing Blank Line separator, <120> field identifier
L:13 M:283 W: Missing Blank Line separator, <130> field identifier
L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:20 M:283 W: Missing Blank Line separator, <160> field identifier
L:22 M:283 W: Missing Blank Line separator, <210> field identifier
L:26 M:283 W: Missing Blank Line separator, <220> field identifier
L:32 M:283 W: Missing Blank Line separator, <400> field identifier
L:53 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:64 M:283 W: Missing Blank Line separator, <220> field identifier
L:70 M:283 W: Missing Blank Line separator, <400> field identifier
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:203 M:283 W: Missing Blank Line separator, <400> field identifier
L:222 M:283 W: Missing Blank Line separator, <220> field identifier
L:226 M:283 W: Missing Blank Line separator, <400> field identifier
L:291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:302 M:283 W: Missing Blank Line separator, <220> field identifier
L:305 M:283 W: Missing Blank Line separator, <400> field identifier
L:396 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:450 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:462 M:283 W: Missing Blank Line separator, <220> field identifier
L:466 M:283 W: Missing Blank Line separator, <400> field identifier
L:511 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:542 M:283 W: Missing Blank Line separator, <220> field identifier
L:546 M:283 W: Missing Blank Line separator, <400> field identifier
L:547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:557 M:283 W: Missing Blank Line separator, <220> field identifier
L:561 M:283 W: Missing Blank Line separator, <400> field identifier
L:562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:564 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:572 M:283 W: Missing Blank Line separator, <400> field identifier
L:599 M:283 W: Missing Blank Line separator, <220> field identifier
L:603 M:283 W: Missing Blank Line separator, <400> field identifier
L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:606 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:614 M:283 W: Missing Blank Line separator, <220> field identifier
L:618 M:283 W: Missing Blank Line separator, <400> field identifier
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:631 M:283 W: Missing Blank Line separator, <220> field identifier

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/981,649

DATE: 11/02/2001

TIME: 15:12:27

Input Set : A:\37665seq.txt

Output Set: N:\CRF3\11022001\I981649.raw

L:633 M:283 W: Missing Blank Line separator, <400> field identifier
L:639 M:283 W: Missing Blank Line separator, <220> field identifier
L:641 M:283 W: Missing Blank Line separator, <400> field identifier
L:647 M:283 W: Missing Blank Line separator, <220> field identifier
L:649 M:283 W: Missing Blank Line separator, <400> field identifier
L:655 M:283 W: Missing Blank Line separator, <220> field identifier
L:657 M:283 W: Missing Blank Line separator, <400> field identifier
L:663 M:283 W: Missing Blank Line separator, <220> field identifier
L:665 M:283 W: Missing Blank Line separator, <400> field identifier
L:671 M:283 W: Missing Blank Line separator, <220> field identifier
L:673 M:283 W: Missing Blank Line separator, <400> field identifier
L:679 M:283 W: Missing Blank Line separator, <220> field identifier
L:683 M:283 W: Missing Blank Line separator, <400> field identifier
L:746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:752 M:283 W: Missing Blank Line separator, <220> field identifier
L:754 M:283 W: Missing Blank Line separator, <400> field identifier
L:760 M:283 W: Missing Blank Line separator, <220> field identifier
L:762 M:283 W: Missing Blank Line separator, <400> field identifier
L:768 M:283 W: Missing Blank Line separator, <220> field identifier
L:770 M:283 W: Missing Blank Line separator, <400> field identifier
L:776 M:283 W: Missing Blank Line separator, <220> field identifier
L:778 M:283 W: Missing Blank Line separator, <400> field identifier
L:779 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:22
L:784 M:283 W: Missing Blank Line separator, <220> field identifier
L:787 M:283 W: Missing Blank Line separator, <400> field identifier
L:909 M:283 W: Missing Blank Line separator, <220> field identifier
L:988 M:283 W: Missing Blank Line separator, <220> field identifier
L:1013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1021 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1024 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1027 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1030 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1033 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1036 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1039 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1042 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1045 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1048 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1051 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1054 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1057 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1060 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1063 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1067 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1070 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1073 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1076 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1079 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1082 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/981,649

DATE: 11/02/2001

TIME: 15:12:27

Input Set : A:\37665seq.txt

Output Set: N:\CRF3\11022001\I981649.raw

L:1085 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1088 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1091 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1094 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1097 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1100 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1112 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1121 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:1220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1231 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1234 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1237 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1240 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1243 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1246 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1249 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1252 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1255 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1258 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1261 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1264 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29
L:1267 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29